

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2003, 22:38:40 ; Search time 12 Seconds
(without alignments)
1779.177 Million cell updates/sec

Title: US-10-098-602A-2

Perfect score: 2376
Sequence: 1 MTITYDELNMLIRNGKIDTV.....INFSKQVTDWELNGFNRY 454

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|----------------------|
| 1 | 880.0 | 100.0 | 135 | GLNA_THEMA | P35205 Thermotoga |
| 2 | 466.0 | 19.6 | 443 | GLNA_CLOSA | P10656 Clostridium |
| 3 | 464.0 | 19.5 | 446 | GLNA_LACIA | Q9cd19 Lactococcus |
| 4 | 443.0 | 18.6 | 446 | GLNA_METVO | P21154 methanococ |
| 5 | 442.5 | 18.6 | 443 | GLNA_BACSU | P12425 bacillus su |
| 6 | 424.5 | 17.9 | 446 | GLNA_STAMW | O59812 staphylococ |
| 7 | 423.0 | 17.8 | 446 | GLNA_STAMW | O99u95 staphylococ |
| 8 | 412.0 | 17.3 | 445 | GLNA_LACDE | P45627 lactobacilli |
| 9 | 411.5 | 17.3 | 443 | GLNA_BACCE | P19064 bacillus ce |
| 10 | 400.5 | 16.9 | 446 | GLNA_METMP | O59648 methanococ |
| 11 | 398.5 | 16.8 | 454 | GLNA_METMP | O60182 methanococ |
| 12 | 395.0 | 16.6 | 442 | GLNA_METTH | O27612 methanobact |
| 13 | 393.5 | 16.6 | 446 | GLNA_METTH | O10378 mycobacteri |
| 14 | 391.0 | 16.5 | 443 | GLNA_PYRKO | O08467 pyrococcus |
| 15 | 389.5 | 16.4 | 439 | GLNA_PYRAB | O9uy99 pyrococcus |
| 16 | 389.5 | 16.4 | 439 | GLNA_PYRAB | O05907 pyrococcus |
| 17 | 387.5 | 16.3 | 454 | GLNA_HALVO | P43386 halobacteri |
| 18 | 386.5 | 16.3 | 454 | GLNA_HALVO | O9nh12 halobacteri |
| 19 | 386.0 | 16.2 | 491 | GLNA_ARCFU | O29313 archaeoglob |
| 20 | 381.5 | 16.1 | 439 | GLNA_PYRMO | P36887 pyrococcus |
| 21 | 376.0 | 15.8 | 443 | GLNA_PYRMO | O58097 pyrococcus |
| 22 | 353.0 | 14.9 | 435 | GLNA_RHIME | O87393 rhizobium m |
| 23 | 341.0 | 14.4 | 472 | GLNA_RHIME | P78061 escherichia |
| 24 | 330.5 | 13.9 | 469 | GLNA_AQUAE | O66514 aquifex aeo |
| 25 | 330.0 | 13.9 | 435 | GLNA_RHIMP | P31592 rhizobium l |
| 26 | 327.0 | 13.8 | 471 | GLNA_SULSO | P23794 sulfolobus |
| 27 | 312.0 | 13.1 | 469 | GLNA_STRRP | P73758 streptomyce |
| 28 | 310.5 | 13.1 | 474 | GLNA_ANASP | P00964 anabaena sp |
| 29 | 308.5 | 13.0 | 474 | GLNA_FRALP | P46033 frankia aln |
| 30 | 303.0 | 12.8 | 478 | GLNA_MYCTU | O10377 mycobacteri |
| 31 | 302.0 | 12.7 | 470 | GLNA_FREDI | P33035 firemycelia d |
| 32 | 301.0 | 12.7 | 469 | GLNA_STRVR | O05342 streptomyce |
| 33 | 300.5 | 12.6 | 473 | GLNA_SULAC | O9hh09 sulfolobus |

| | | | | | | |
|----|-------|------|-----|---|------------|---------------------|
| 34 | 299.0 | 12.6 | 469 | 1 | GLNA_STRCO | P15106 streptomyce |
| 35 | 293.0 | 12.3 | 473 | 1 | GLNA_SYNRP | P28605 synecchococ |
| 36 | 287.5 | 12.1 | 469 | 1 | GLNA_RHIME | O59747 rhizobium m |
| 37 | 287.0 | 12.1 | 472 | 1 | GLNA_HAEIN | P43794 haemophilus |
| 38 | 283.0 | 11.9 | 468 | 1 | GLNA_METCA | P15124 methylococ |
| 39 | 283.0 | 11.9 | 472 | 1 | GLNA_PASWU | O9cd12 pasteurilla |
| 40 | 280.0 | 11.8 | 468 | 1 | GLNA_AZOBK | P10583 azospirillum |
| 41 | 278.5 | 11.7 | 468 | 1 | GLNA_VIBAL | P19504 vibrio algi |
| 42 | 276.0 | 11.6 | 467 | 1 | GLNA_AZOCI | P22248 azotobacter |
| 43 | 270.0 | 11.4 | 468 | 1 | GLNA_AZOCI | P94126 azorhizobiu |
| 44 | 269.0 | 11.3 | 481 | 1 | GLNA_HELPY | P94845 heliobacter |
| 45 | 267.5 | 11.3 | 469 | 1 | GLNA_PROVU | P28786 proteus vul |

ALIGNMENTS

RESULT 1
ID GLNA_THEMA STANDARD; PRT; 439 AA.

AC P36205; DT 01-JUN-1994 (Rel. 29, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS).

GN GLNA OR TM0943.

OS Thermotoga maritima.

OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.

OX NCBI_TaxID=2336;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109;

RA MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Uterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima."

RT Nature 393:323-329(1999).

RL

CC CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate +

CC L-glutamine.

CC -1- SUBUNIT: Oligomer of 12 subunits arranged in the form of two

CC hexagons (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.

downscaled
active

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EMBL; X60160; CA44729.1; -

EMBL; A6001758; AAD36024.1; -

PIR; B72313; B72313.

HSSP; P06201; ILGR.

TIGR; TM0943; -

InterPro; IPR001691; GLN_synth.

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 20.2% | Score 480; | DB 1; | Length 439; |
| Best Local Similarity | 29.9% | Pred. No. 1.1e-30; | | |
| Matches 138; | Conservative 73; | Mismatches 209; | Indels 42; | Gaps 9; |

Oy 3 TYDELDNNIRNGKIDTVLACVDMOGRMLKRTGRHFLGDOCKLISTSTFYAVTIE 61
 Db 1 MTEITIKRIEENNAFIRLOFTDINGTL-----KOLEITPVFLESMBD 45
 Oy 62 GIAGGGEYISS-VDTGYSDCHLCAIDNSLHLLPWS-EGA-----VLAISPNHVTSTEDP 114
 Db 46 GIMPDGSSIEGFEVRIEESDMYLKFPVLDPAVLFWTVDCAKSARVICDYVTP--DGKPF 101
 Oy 56 155 54
 115 FCSBPVILMOQERLANLTKGLFASLEPNLENEYKASQCHMKNLKTAOPHOOMNI 174
 Db 102 EGDPRRLRMRMEKABOLQYTPYAGEEMGFPIIPNEKEBVEBEJLD-----HGCFID 155
 Oy 175 SASGJETERMSVRNKLBEAGILMEHTHEFLESOHELNFPADPLTMADRHIIAAGVRA 234
 Db 156 LPLSKVEIRDIALIEMKGIIVETHDHFVARSQHPVBYDTPRLRTADNAQTVLVIK 215
 Oy 235 ENABOSGMVATPFAKISSTRALGNACGITHNSLODAETBEKAFYONDYEGNSTIARWING 294
 Db 216 TMAIFGHYATMPKPPGYNGSSGGMVHNSL--FRDCKAFYDPDPLJGSKELRYFVVG 273
 Oy 295 ILKYYEATFYFASVSYKRLDPLTFAPKCMALDNRSTASAPLCSKSEGINVELRIG 354
 Db 274 ILKHAKALAAVNPNTINSYKRLVPGYEAFLYICMSGNBRBALRIPARAKATRIEESP 333
 Oy 335 GADLNDYLAFSATITANGISIEBEKLEBPFPASGNVTH-----DKELPEFPNSONATH 407
 Db 334 DPCSCNYILFAALIAAGLDGIIINKIEBPAAVEENIYHMTSERBELNIESLPGLKEAVE 393
 Oy 408 LKESKMLKTBEGEKLILHYVNAANYEINEPSQVDMWENO 449
 Db 394 ELKQDVITIDALGEHILPEKFEVAEKDWEKSTYVIMNEJOR 435

| | | | |
|------------|---|-----------------------------------|--------------|
| RESULT 2 | | | |
| GLNA_CLOSA | | | |
| ID | _GLNA_CLOSA | STANDARD; | PRT: 443 AA. |
| AC | P10656; | | |
| DT | 01-JUL-1989 | (Rel. 11, Created) | |
| DT | 01-JUL-1989 | (Rel. 11, Last sequence update) | |
| DT | 16-OCT-2001 | (Rel. 40, Last annotation update) | |
| DE | Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase). | | |
| GN | GLNA. | | |
| OS | Clostridium saccharobutylicum. | | |
| OC | Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; | | |
| OC | Clostridium. | | |
| OX | NCBI_TaxID=169679; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=P262; | | |
| RX | MEDLINE=88086901; PubMed=2891680; | | |
| RA | Janssen P.J., Jones W.A., Jones D.T., Woods D.R.; | | |
| RT | Molecular analysis and regulation of the glnA gene of the Gram- | | |
| RT | positive anaerobe Clostridium acetobutylicum. | | |
| RL | Bacteriol. 170:400-408(1988). | | |
| CC | -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate + | | |